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Listing first 45 summaries
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49
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Copyright (c) 1993 - 2004 Compugen Ltd
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21.381 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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	Aag48926	Adk16325	Aag92924	Abb71784	Abb48690	Aaw15763	Abg03180	Abg19995	Abm72169	Adf07002	Abu40604	Abu19282	Abp26836	Adf04069	Abu41142	Adf04191	Ada35435	Abb58253	Abm71532	ADm / MDA

ALIGNMENTS

RESULT 1 ABG32304

Homo sapiens. HLA-A2 associated immunogenic 05-NOV-2002 ABG32304 standard; peptide; 9 WO200246416-A2 ABG32304; (first entry) peptide from human Topoisomerase II. B

Human; immunogen; epitope; HLA-A1; human leukocyte antigen; CTL; cytotoxic Y lymphocyte; cytostatic; cancer; colorectal carcinoma; ovarian carcinoma; lung carcinoma; prostate carcinoma; vaccine; tumour; HLA-2; passive immunotherapy; topoisomerase II.

13-JUN-2002.

04-DEC-2001; 2001WO-US047290

04-DEC-2000; 2000US-0251022P. 20-DEC-2000; 2000US-0256824P.

(ARGO-) ARGONEX INC.

Ramakrishna V, Ross M, Philip <u>بح</u>

WPI; 2002-619021/66.

New and immunogen useful as a vaccine for inducing cytotoxic T-lymphocyte, for diagnosing, preventing or treating cancer e.g. ovarian carcinoma.

Claim 1; Page 50; 60pp; English.

whose amino acid sequence comprises an epitopic peptide, does not include MAGE 4 or MFG-E8 proteins, or consists of Mage D protein or its immunologically active fragment. Also included are a polynucleotide encoding the immunogen or its complement, a vector comprising the polynucleotide, a mammalian cell comprising the vector and expressing the polynucleotide, a vaccine composition comprising the immunogen and an antibody specific for the immunogen. The immunogen is useful for inducing a cytotoxic T lymphocyte (CTL) in vitro that is specific for a tumour cell expressing human leukocyte antigen (HLA)-Al or A2. The immunogen is useful for inducing a CTL response when administered to a subject. A The invention relates to an immunogen comprising an isolated polypeptide

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RESULT 2
ABG22395
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Matches
The invention relates to isolated polynucleotide (I) and polypeptide (I) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
                                                                                                                                                                                                                                              diagnostics, forensics, responsible for genetic biodiversity.
                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mappi and in recombinant production of (II). The polynucleotides are also in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is

for generating

quantitating

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain

mapping,

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ARESULT 3
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XX ABG2
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XX Huma
XW Huma
XW Food
OS Homc
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RESULT 4
ADE61230
ID ADE6230
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PR 14-
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01-NOV-2001;
26-NOV-2001;
The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268312/26.
GENBANK; P41516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide in tissue, as molecular weight markers and as a foosupplement. (II) and its binding partners are useful in medical of sites expressing (II). (I) and (II) are useful for treating of sites expressing (II).
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                                                                                                                                                                                                                                                                                                                                                                                                                   two or more isolated polypeptides, treating pain in an animal.
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Pred. No. 1.4
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RESULT 5
ADD44993
ID 4AP93
AC ADD4
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AC Rat;
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                                                                                                                                                                                                                                               New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; P41516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO )
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Pred. No. 2;
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ine invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a

Claim 1; Page; 1017pp; English.

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RESULT 6
ADN95295
ID ADN9
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Best Local S
Matches
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or
                                                                                                                                                                                                                                                                N-PSDB; ADN95296.
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                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                             Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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9; Conserv
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                                                                                                                                                                                  217; 176pp;
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Pred. No. 2;
0; Mismatches
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                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                             Saharinen P,
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F S

Claim 2; SEQ ID NO 2593; 266pp + Sequence Listing; English

New isolated tumor colon polynucleotide and polypeptide, useful for the diagnosis, prevention and/or treatment of cancer, in particular colon

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RESULT 7
ABP67994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises cidentifying a human subject with lymphoedema and with a mutation in at CC least one allele of a gene encoding a LEC protein, where the mutation CC correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a CC composition comprising a lymphatic growth agent selected from VEGF-C or CC VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, CC vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood cells or lymphatic endothelial cells, in treating hereditary CC lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a CC endothelial crop the differential modulation of blood vessel endothelial cell or lymphatic vessels endothelial cell growth or differentiation. The CC lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a CC LEC gene or of other diseases and cancer metastasis via the lymphatic cexpressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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06-FEB-2001; 2001US-0267011P
28-MAR-2001; 2001US-0279670P-
10-JUL-2001; 2001US-0304037P
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer related polypeptide SEQ
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                                                                                          WPI; 2002-608400/65.
N-PSDB; ABV89274.
                                                                                                                                          Stolk JA,
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                      colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; tumour; gene therapy; vaccine
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                                                                                                                                          Meagher MJ,
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RESULT 8
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Best Local
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08-FEB-1999;
16-SEP-1999;
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              The present invention relates to a method of detecting the presence of ovarian cancer in a patient, involving detecting ovarian cancer associated polynucleotides. The method is not only used to detect the presence of cancer, preferably ovarian cancer in a patient, but also is used to stimulate and/or expand T cells specific for an ovarian tumour protein. The sequences can be used in vaccines used to treat cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                           (BENS/)
(LODE/)
(MITC/)
                                                                                                                                                                             Example 2; Page 142-145; 188pp; English.
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                                                                                                                                                                                                                                            Composition for detecting and treating specific polypeptide, polynucleotide, I
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                                                                                                                                                                                                                                                                                                                                                                                                         (KING/)
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9; Conserv
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MITCHAM J L.
KING G B.
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ng cell.
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ilarity 100.0%;
Conservative (
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99US-00246429.
99US-00397787.
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18
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ovarian
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Pred. No.
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associated
                                                                                                                                                                                                                                            y ovarian cancer, comprises a T cell population, or antigen
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RESULT 10
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ABU56492 standard;

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Best Local S
Matches 9
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Best Local
                                                                                                                                  The invention relates to a target protein fused with a polypeptide having an amino acid sequence containing an epitope of anti-human type II DNA topoisomerase alpha antibody and the DNA encoding it. The sequences can be used in a method for the detection or the determination of a target protein in which the target protein is detected or determined by using the reactivity between the target protein and the above fused protein as the index, and also in a method for the purification of a target protein in which the above fused protein is contacted to anti-human type II DNA topoisomerase alpha antibody carried on a solid carrier. This sequence represents an anti-human type II DNA topoisomerase alpha monoclonal
                                                                                                  Sequence 1531 AA;
                                                                                                                                                                                                                                                                            Disclosure; Page 20-23; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                   Detection or determination of a protein, a fused protein, vector, purification of a target protein, a solid carrier, peptide, a kit for the detection or determination.
                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2000; 2000JP-00394675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; type II DNA topoisomerase alpha antibody; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-human type
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                                                Similarity 9; Conserv
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9; Conserv
FLYDDNORV
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                                                Conservative
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                                                Score 49; DB
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Pred. No.
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RESULT 11
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                                                                                                                                                       Query Match
Best Local S
Matches 9
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09-NOV-2001;
13-NOV-2001;
29-NOV-2001;
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                                                                                                                                                                                                                        Sequence 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression in lung
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9; Conserv
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ilarity 100.0%;
Conservative (
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; 2001US-0290492P.
; 2001US-039245P.
; 2001US-0350666P.
; 2001US-0334370P.
; 2002US-0372246P.
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                                                                                                                                                     Score 49; DB
Pred. No. 2;
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ABR92156 standard; protein; 1531 AA

Human Protein P11388, SEQ ID NO 10426

29-JAN-2004

(first entry)

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RESULT 12
ADD44995
ID ADD44
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AC ADD44
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Matches 9
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13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
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Gannavarapu M,
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9; Conserva
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M, Glatt )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 49;
100.0%; Pred. No.
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K, H
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Hoersch S;
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                                                                                   RESULT 13
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                                     Sequence
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    ADE61232;
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                                         ADE61232 standard; protein; 1531 AA.
                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic ftp.wipo.int/pub/published_pct_sequences.
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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BAYER AG.
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2001US-0333347P.
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828 FLYDDNORV 836

FLYDDNQRV

Matches Query Match Best Local

Similarity

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100.0%; Score 49; 100.0%; Pred. No.

Conservative

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Mismatches

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Gaps

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TOP WILLIAM HITCHE

Length 1531;

Sequence

1531

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cc subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially cc expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the cc compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
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segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEN HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>,
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                                                                                                                                                                                                                                                                                               or prognosis of malignant neoplasia by the detection of at least two markers. The invention may also be useful for the development of cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia such as breast cancer, ovarian cancer, gastric cancer, colon cancer, cesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell lung cancer. The polynucleotides and polypeptides defined in the specification, antisense polynucleotides targeting the polynucleotides, antibodies targeting either one of the polynucleotides or polypeptides, and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of
   06-MAY-2004
                                ADL12474;
                                                                                                                                                                                                                                                         Sequence 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Predicting, diagnosing or prognosing malignant neoplasia by detecting least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wirtz R,
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13-FEB-2003;
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                                                           ADL12474 standard; protein; 1531 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for the prediction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; SEQ ID NO 46; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2003; 2003EP-00010447
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                                                                                                                                                                   FLYDDNQRV 9
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llarity 100.0%;
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Search completed: December 29, Job time : 155 secs

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cc ligand that specifically binds a cDNA. The sample is from a subject with comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human protein which is differentially expressed in steroid-induced CJA liver cells. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html.
Matches
                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a combination comprising cDNAs that are differentially expressed in response to strend treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high a throughput method of screening molecules or compounds to identify a lighed that conditions in the control of screening molecules or compounds to identify a lighed that conditions in the control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds to identify a light control of screening molecules or compounds.
                                                                                                               Sequence 1531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hep-comprises cDNAs that are differentially expressed in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 203; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000; 2000US-0240409P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-470-179-30
US-09-270-767-43224
US-09-328-352-6722
US-09-543-681A-4476
US-09-543-681A-7287
US-09-543-681A-7287
US-09-543-681A-7287
US-09-262-653A-10
US-09-262-653A-10
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US-08-765-179B-19
US-08-765-179B-19
US-08-765-179B-20
US-09-490-070A-20
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Sequence 203, App
Sequence 30, Appl
Sequence 476, Ap
Sequence 4354, Ap
Sequence 4354, Ap
Sequence 10, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 65, Appli
Sequence 4, Appli
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63.3	63.3	63.3	64.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	6/.3
112	112	99	254	1584	528	359	304	286	242	234	109	109	109	109	109	109	206
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US-09-315-574-39	US-08-665-202-39	US-09-107-532A-5802	US-09-266-965-123	US-09-251-645-6	US-09-248-796A-17909	US-09-248-796A-14544	US-09-248-796A-16060	US-09-489-039A-10682	US-08-884-569A-5	US-09-372-425A-4	US-09-490-153-51	US-09-490-153-32	US-09-490-070A-51	US-09-490-070A-32	US-09-025-769B-51	US-09-025-769B-32	05-08-101-846-2
Sequence 3	Sequence 3	Sequence 5	Sequence 1	Sequence 6	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 5	Sequence 4	Sequence 5	Sequence 3	Sequence 5	Sequence 3	Sequence 5	Sequence 3	sequence 2
•	39, Appl	5802, Ap	123, App	6, Appli	17909, A	14544, A	16060, A	10682, A	, Appli	, Appli	51, Appl	2, Appl	51, Appl	•	il, Appl	32, Appl	TIGGA .:

# ALIGNMENTS

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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
ITILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
SECOND SECON
                                                                                                                                                                                                                                                                                                                                                                                                        PATENT NO. 5645994
GENERAL INFORMATION:
APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/08470179 Patent No. 5645994
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask, Britt and Rossa
STREET: P.O. Box 2550
                                                                                                                                                                               STREET: P.O. Box 2550
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 FLYDDNORV 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FLYDDNORV 9
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Similarity 100.0%;
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Pred. No.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

MEDIUM TYPE:

Floppy disk

ATTORNEY/AGENT INFORMATION:

FILING DATE: CLASSIFICATION: 435

APPLICATION NUMBER:

US/08/470,179

TELEFAX: 801-531-9168 INFORMATION FOR SEQ ID NO:

30:

TELEPHONE:

801-532-1922

TELECOMMUNICATION INFORMATION: NAME: Sweigert Ph.D, Susan B. REGISTRATION NUMBER: 36,289 REFERENCE/DOCKET NUMBER: 2601

2601

SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid

FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Homo sapiens sapiens

MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO

STRANDEDNESS:
TOPOLOGY: not relevant

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Query Match
Best Local Similarity
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US-09-270-767-43224
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                                                                                                            US-09-328-352-6722
                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Drosophila melanogaster US-09-270-767-43224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-470-179-30
                                                      Sequence 6722, Appli
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
LENCTH. 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43224, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 324
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                                                                                           Application US/09328352
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77.8%;
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US-09-543-681A-4476
; Sequence 4476, Application US/09543681A
; Patent No. 6605709
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US-09-543-681A-4354
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                                                                       US-09-543-681A-4354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4476
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                        SEQ ID NO 4354
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Matches
                Query Match
Best Local Similarity
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                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2000-04
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GTC99-03PA
                                                                                    LENGTH: 233
TYPE: PRT
ORGANISM: Proteus mirabilis
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TYPE: PRT
ORGANISM: Proteus mirabilis
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Local Similarity 66.7%;
nes 6; Conservation
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6; Conservative
                71.4%;
75.0%;
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                Score 35; DB
Pred. No. 54;
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Pred. No. 2.7e+02;

    Mismatches

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Pred. No. 29;
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                                 Length 233;
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Indels
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US-08-580-545B-10
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US-09-543-681A-7287
                                                                                                 APPLICATION NUMBER: US/08/580,545B
PILING DATE
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/783-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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SEQ ID NO 7287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: DIAGNOSTICS AND THERAF FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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                                                                TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                            SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acid
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Koshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YOShihiko, Maĕkawa
APPLICANT: Randy, Allen
TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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. 6605709
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5932713
               amino acid
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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RESULT 10
US-09-248-796A-23295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-580-545B-10
                                                                                                                                                                                                                                                                                                           US-09-262-653A-10
                                               Sequence 23295, Application US/09248796A Patent No. 6747137
GENERRAL INFORMATION:
APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACLD AMD AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICATITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION UNMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/262,653A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yoshihiko, Ma
APPLICANT: Randy, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 601 Thirt
CITY: Washington
                                                                                                                                                                                                                                 69.4%;
Local Similarity 62.5%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                       LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ZIP: 20005
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Susumu, Nishiguchi
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Pred. No. 83;
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Pred. No.
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US-08-765-179B-19
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US-09-248-796A-23295
                                                                                                                                  US-08-765-179B-19
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION NUMBER: US/08/765,179B
FILING DATE: 14-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23295
                                                                 Matches
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Best Local
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LENGTH: 64 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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APPLICANT: STEINBACHER, Stefan
APPLICANT: STEINBACHER, Stefan
APPLICANT: STEINBACHER, STEFAN
APPLICANT: STEINBACHER, STEFANTES
                                                                                                                                                TOPOLOGY: 15
MOLECULE TYPE:
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                                                                                Local
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17 IYDDNKK 23
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                              2 LYDDNQR 8
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                                                               67.3%; ilarity 71.4%; Conservative
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                                                               Score 33; DB Pred. No. 33; 2; Mismatches
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Pred. No. 1.6e+02;
0; Mismatches 0;
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                                                                                            Length 64;
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RESULT 12

US-08-468-671-10

Sequence 10, Application US/08468671 Patent No. 5648077

GENERAL INFORMATION:
APPLICANT: Ostberg,
TITLE OF INVENTION:

Lars G.
PRODUCTION OF HUMAN MONOCLONAL

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RESULT 13
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                                                                                                                                 Best Local Similarity
Matches 5; Conserve
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                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTONNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/676,036
APPLICATION NUMBER: US 07/676,036
                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
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APPLICANT: Ostberg
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FILING DATE: 15-UN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 11-MAY-1
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TITLE OF INVENTION: P
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                   MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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CITY: San Francisco
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                                                         47 VYDDNER 53
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11-MAY-1988
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PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS
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                                                                                                                                                     Score 33; DB 1; Length 108; Pred. No. 57;
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                                                                                                                                       Mismatches
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                                                                                                                           Sequence 20, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                         Patent No.
                                                                    GENERAL INFORMATION:
APPLICANT: Knappi
APPLICANT: Pack,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 326-2400
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FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-MAY-1988 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        APPLICANT:
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                                       APPLICANT:
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FILING DATE: 27-MAR-1991
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Ilag, Vic
Ge, Liming
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Moroney, Simon
Plueckthun, Andreas
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71.4%;
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RESULT 15
US-09-490-070A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09490070A Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-909 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Es
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/490,070A
                                                                                                                                                                                                                    Moroney, Šimon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Foly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 IYDDNKR 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYDDNQR
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                                                                                                                                                                          STATE: D.C.
                                                                                                                                                                                         STREET: 1666 K Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
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Ge, Liming
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PRIOR DATE: 24-Jan-2000

PRIOR APPLICATION NAME:

APPLICATION NUMBER: BP 95 11 3021.0

PILING DATE: 10-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REGISTRATION NUMBER: 37629-0005

TELEPHONE: (202) 912-2000

TELEPHONE: (202) 912-2000

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: smino acid

TYPE: smino acid

TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-490-070A-20

Query Match
Best Local Similarity 71.4%; Pred. No. 57;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps

Query Match
Best Local Similarity 71.4; Pred. No. 57;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps

Qy 2 Lyddnor 52

Search completed: December 29, 2004, 16:31:56

Search completed: December 29, 2004, 16:31:56
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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       92:
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Q8Y714
Q720C9
AAT04085
Q9N4W3
Q2753W7
TOP2_CAEEL
Q7R8R3
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TP2B_CRILO
TP2B_MOUSE
Q7TQG4
TP2B_HUMAN
TP2B_CHICK
Q7ZXS2
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TP2A_HUMAN
TP2A_PIG
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Q9DFB7
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Q63177
Q6W6M6
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P41516 cricetulus
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P11388 homo sapien
O42130 gallus gall
O94677 gallus gall
O71uh4 homo sapien
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Q6w6m6 homo sapien
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RESULT 2
Q63177
ID Q631
AC Q631
DT 01-N
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DE 'DNA
DE 'DNA
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Q63177 PRELIMINARY; PRT; 214 AA. Q63177; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) ONA topoisomerase IIB' (Fragment).

Rattus norvegicus (Rat).

Oy Ma	DR DR DR SQ	DR RT T P R R R R R R R R R R R R R R R R	RESULT Q63176 ID Q63176 AC Q0 DT C1 DT C1 DT C1 DT C1 OC EN	
Query Match Best Local Matches 1	GO; GO:0005524 GO; GO:0003677 GO; GO:0003918 GO; GO:0016853 GO; GO:0006265 InterPro; IPRO Pfam; PF00521; ProDom; PD0007 SMART; SM00434 Isomerase. NON TER 21 SEQUENCE 214	SEQUENCE F. STRAIN-Spr. MEDLINE-93 TButsui K. Inoue Y.; "Molecular isoforms a. J. Biol. C. EMBL; D140	IJT 1  176  Q63176; PRELII Q63176; CTYEM 01-NOV-1996 (TYEM 01-NOV-1996 (TYEM 01-OCT-2003 (TYEM 01-OCT-2003 (TYEM 01-OCT-2013 (TYEM 01-OCT-	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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larity Conserv DDNQRV 	005524; F:DNA 003677; F:DNA 003918; F:INA 016853; F:ISOM 016853; F:ISOM 006225; P:DNA TER002205; DNA TER002742; DNA ED000742; DNA M00434; TOP4C; E. 1 1 1 214 AA; 24	SEQUENCE FROM N.A. STRAINSprague-Dawley; TISSUB-Br MEDLINE=3336632; PubMed=8395528 TButsui K., Tsutsui K., Okada S. Tsutsui K., Tsutsui K., Okada S. Inoue Y.; "Molecular cloning of partial cD "Molecular cloning of partial cl isoforms and their differential isoforms and their 19076-19083(1 J. Biol. Chem. 268:19076-19083(1 EMBL; D14045; BAA03132.1;	PRELIM (Treme (Treme (Treme (Treme ) merase gicus letazoa letazoa	77.5.5 75.5.5 75.5.5 75.5.5 75.5.5 75.5.5 75.5.5
100 100 ive	F:ATP binding; F:DNA binding; F:DNA topoisome: F:isomerase act: F:isomeras	.ey; T hubMed K., K., of pa diffe 19076	IINARY; Lirel. 01, C: Lirel. 01, L: Lirel. 25, L: (IIA' (Fraguera); (Cat).; Chordata; ; Rodentia;	1095 67 67 80 80 80 80 80 80 80 80
0 4	binding; binding; topoisom erase ac topologi NA_topoi oisoIV; topoisoI 1.	rissum. Med=8395 , Okada partial Eferentia )76-1908 2.1;	01, 01, 25, (Fra data	000000000000000
; Score 49; DB 2; Length 2; Pred. No. 0.19; 0; Mismatches 0; Indels	F:ATP binding; IEA. F:DNA binding; IEA. F:DNA binding; IEA. F:DNA topoisomerase (ATP-hydrolyzing) F:isomerase activity; IEA. P:DNA topoisoTV. 205; DNA_topoisoTV. NA topoisoTV; 1. ; DNA_topoisoTV; 1. TOP4C; 1.  1 1 214 214 A; 24172 MW; 46A28AIDEA188A5A CRC64;	ain; , Watanabe M., Shohm , Watanabe M., Shohm NAs for rat DNA topo expression in brain 993).	PRT; 214 AA. reated) ast sequence update) ast annotation update) ment). Craniata; Vertebrata; Sciurognathi; Muridae;	Q7RSJ8 Q6ZBR4 BAD10035 O80089 Q6R830 Q9BDF4 Q6GAN4 Q6GGN4 Q6GGN4 Q9NWHB Q911KB AAR87916 Q9MER3 Q8SDL7 ALIGNMENTS
1214; ils 0; Gaps 0;	activity; IEA.	hohmori T., Seki S., topoisomerase II ain development.";	Euteleostomi; Murinae; Rattus.	07rsj8 plasmodium 06z8r4 oryza sativ Bad10035 oryza sativ Bad10035 oryza sativ 080089 staphylococ 06r830 bacteriopha 09b0£4 staphylococ 06gan4 staphylococ 06gf76 staphylococ 06gf76 staphylococ 06gf76 staphylococ 06gf76 staphylococ 06gf76 staphylococ 06gf76 staphylococ 06gf78 staphylococ 0931k8 staphylococ 0931k8 staphylococ 031k8 staphylococ 0Ar87916 bacteriop 09mbr3 staphylococ 0Bsd17 staphylococ 0Bsd17 staphylococ

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ACLE

SEQUENCE FROM N.A.

A Chen G., Zhang W.G., Fu J., Cao X.M.,

AA Han Y.H., Li F.Y., Liu X.P., Yao L.B.;

AA Han Y.H. (MAY-2003) to the EMBL/GenBank/DDBJ dat

DR Submitted (MAY-2003) to the EMBL/GenBank/DDBJ dat

DR InterPro; IPR002205; DNA topoisoIV.

DR Pfam; PP00521; DNA topoisoIV; 1.

ProDom; PD000742; DNA topoisoIV; 1.

ProDom; PD000742; DNA topoisoIV; 1.

ProDom; P000434; TOP4C; 1.

PROPOSE CM00434; TOP4C; 1.

PROPOSE CM00434; TOP4C; 1.

PROPOSE CM00434; TOP4C; 1.
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ID W6M6
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SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-93366832; PubMed-8395528;
MEDLINE-93366832; Wantsui K., Okada S., Wa
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00521; DNA_topo
ProDom; PD000742; DNA_topo
SMART; SM00434; TOP4c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of partial cDNAs for rat isoforms and their differential expression J. Biol. Chem. 268:19076-19083(1993).
EMBL; D14046; BAA03133.1; -.
PIR; B48536; B48536.
  AAR16193
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05-JUL-2004
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003918; F:DNA topolsomerase (ATP-hydrolyzing)
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0016853; F:DNA topological change; IEA.
InterPro; IPR002205; DNA topological.
PRO0521; DNA topological.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Best Local S
Matches
[4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20499374, PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibatarinci P., Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8CCE5;
Q8CCE5;
01-MAR-2003
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 15 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:8030493B08 product:topoisomerase (DNA) 1
alpha, full insert sequence. (Fragment).
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Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085560; Pubmed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-99279253; PubMed-10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome t 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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01-APR-2004 (TrEMBLrel.
01-APR-2004 (TrEMBLrel.
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STRAIN=C57BL/6J; TISSUE=Testis;
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Mammalia; Eutheria;
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SEQUENCE 373 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium,
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9; Conserv
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AA; 42817 MW
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Rodentia;
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Pred.
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Catarrhini;
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                                                                   new genes.";
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10:1617-1630(2000)

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RC STRAIN=C57BL/6J; TISSUE=Testis;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

RA Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Hori F., Imotani K., Kojina Y., Kondo S., Konno H., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Katoh H., Kawai J., Kojina Y., Kondo S., Konno H., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RA Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

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RA Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RA Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RA Tagawa A., Toya T., 
                                                                                                                                            Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0040016; P:embryonic cleavage; IN InterPro; IPR003957; CBFA, NFYB topis. InterPro; IPR011558; DNA_Gyrase B. InterPro; IPR011558; DNA_topoisoII. InterPro; IPR001241; DNA_topoisoIV. Pfam; PR00521; DNA_topoisoIV. Pfam; PR006152; CDATSUBUNTA. PRINTS; PR00615; CCAATSUBUNTA. PRINTS; PR00418; TP12FAMILY. PRODOM; PD149633; DNA_Gyrase B; 1. ProDom; PD10974; DNA_topoisoIV; 1. SMART; SM00434; TOP2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Jawa M., Hayashizaki Y., Okazaki Y., Muramatsu M., Sawa K., Tanaka T., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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MEDLINE=20530913; PubMed=110768
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                                                                        FLYDDNORV
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                                                                                                                                                Conservative
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RESULT 6 TP2A\_CRIGR

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                                                                                                                               Matches
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Best Local
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Pfam; PPO0521; DNA_CODASOIV; 1.
Pfam; PPC0518; HATPBAS C; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TP12FAMILY.
PRODOM; PD000742; DNA_COPÓSOIV; 1.
SMART; SM00387; HATPBAS C; 1.
SMART; SM00433; TOP4C; 1.
SMART; SM00433; TOP4C; 1.
SMART; SM00434; TOP4C; 1.
SMART; SM00434; TOP4C; 1.
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P41515;
01-NOV-1995
01-NOV-1995
                                                                                                                                                            NP_BIND
ACT_SITE
VARTANT
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
DNA topoisomerase II, alpha isozyme (BC 5.99.1.3).
Name=TOP2A; Synonyms=TOP2, TOP-2;
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              SEQUENCE
                                                                                                                                                                                                           ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L04607; AAA37023.1; -. PIR; A44406; A44406. HSSP; P06786; 1BJT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ++
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J. Biol. Chem. 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93131977; PubMed=8380592; Chan V.T., Ng S.W., Eder J.F., Schnipper L.E.; myolecular cloning and identification of a point mutation in the topoisomerase II cDNA from an etoposide-resistant Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=93131977;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003957; CBFA NFTB topis.
InterPro; IPR001241; DNA_topoisoIV.
InterPro; IPR002205; DNA_topoisoIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breakage and subsequent rejoining of DNA strands. Topoisomerase I) makes double-strand breaks.

CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

SUBUNIT: Homodimer.

SUBCELLAURAGUS: Eukaryotic topoisomerase I and II can relax both negative and positive supercoils, whereas prokaryotic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relax only negative supercoils. SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Control
827 FLYDDNORV 835
                                                            Similarity 100 9; Conservative
                               FLYDDNQRV
                                                                                                                              1526
                                                                                                                                                                                                      0177; TOPOISOMERASE II; 1.

DNA-binding; Isomerase; Nuclear protein; Topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268:2160-2165(1993).
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493
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                                                                                                                            ATP (Potential).

DNA cleavage (By similarity).

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ANTINEOPLASTIC AGENTS VP-16 AND
MW; 5FBZDBFBF1CO2929 CRC64;
                                                                             Score 49; DB
Pred. No. 1.8;
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Topoisomerase II
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RESULT 7
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                                                                                                                      Query Match
Best Local
                                                           Matches
                                                                                                                                                                                                                   RGD; 62048; TOP2a.

InterPro; IPRO03594; ATPbind ATPage.
InterPro; IPRO03957; CBFA NPVB top18.
InterPro; IPRO01241; DNA top0180II.
InterPro; IPRO01201; DNA top0180IV.
Pfam; PF00204; DNA gyraseB; 1.
Pfam; PF00521; DNA top0180IV; 1.
Pfam; PF00521; DNA top0180IV; 1.
PRAM; PF00518; HATPage c; 1.
PRAM; PRO0615; CCAATSUBUNTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homogimer.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both negative and positive supercoils, whereas prokaryotic enzymes negative and positive supercoils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vi-NOV-1995 (Rel. 32, Last sequence update) 05.JUL-2004 (Rel. 44, Last annotation updat DNA topoisomerase II, alpha isozyme (EC 5.9 Name=Top2a; Synonyms=Top2, Top-2; Rattus norvegicus (Rat).
                                                                                                                   NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP2A RJ
P41516,
                                                                                                                                                                                                                                                                                                                                         EMBL; Z46372; CAA86496.1; -.
EMBL; Z19552; CAA79611.1; -.
EMBL; Z1955676; -, NOT_ANNOTAT:
HSSP; P06786; 1BJT.
HSSP; P06786; 1BJT.
TGD28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINESprague-Dawley; TISSUE-Testis; MEDLINE=9290677; PubMed=390233; Park S.D. Park S.D. Park S.D. "Nucleotide sequence analysis of the cDNA"
                                                                                                                                                         ProDom; PD000742; DNA_topoisoIV; 1.

PROSITE; PS00177; TOPOISOMERASE II; 1.

ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
                                                                                                                                                                                                           PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chem. Blophys. Res. Commun. 193:787-793(1993). FUNCTION: Control of topological states of DNA by breakage and subsequent rejoining of DNA strands. makes double-strand breaks.
CATALYTIC ACTIVITY: ATP-dependent breakage, passacof double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relax only negative supercoils. SIMILARITY: Belongs to the type II topoisomerase family.
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826
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                                                         9
                                                                         Similarity
                                                                                                                                                                                                           PR00418; TPI2FAMILY.
FLYDDNORV 834
                             FLYDDNORV
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803
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                                                           Conservative
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                                                                       100.0%;
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DNA
MW;
                                                       0
                                                                       Score 49; DB 1;
Pred. No. 1.8;
                                                           Mismatches
                                                                                                                   (Potential).
cleavage (By similarity)
Al961ABBDB1B050F CRC64;
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(EC 5.99.1.
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; Murinae; Rat
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Topoisomerase
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RESULT 8

055079 055079; 01-JUN-1998 01-JUN-1998

(TrEMBLrel. 06, (TrEMBLrel. 06, PRELIMINARY;

Created)
Last sequence update)

PRT;

1526

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RESULT
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ID O5
AC O5
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Carrier New Control of topological states of DNA by transient Colification of DNA strands. Topolsomerase II Commakes double-strand breaks (By similarity).

Circ formalyTIC ACTIVITY: ATP-dependent breakage, passage and rejoining Colification of double-stranded DNA.

Circ formalyTIC ACTIVITY: ATP-dependent breakage, passage and rejoining Colification of double-stranded DNA.

Circ formalyTIC Homodimer (By similarity).

Circ formaly inspative supercoils, whereas prokaryotic enzymes colification of the type II can relax both colification of the type II can relax both colification of the type II topolsomerase family.

EMBL; Y16594; CAA76312.1; -.

DR GO; GO:000524; FATP binding; IEA.

GO; GO:000524; FATP binding; IEA.

GO; GO:0005394; FIDNA topolsomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:0016393; FIDNA topolsomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:001625; P.DNA topolsomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:001625; P.DNA topolsomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:0016394; ATPBIND ATP
                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0615; CCAATSUBUNTA.
PRINTS; PRO0418; TPIZPAMILY.
PRODOM; PD149633; DNA TOPO160IV; 1.
PRODOM; PD000742; DNA TOPO160IV; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00433; TOP2C; 1.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA topoisomerase II alpha (EC 5.99.1.3).
Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99446895; PubMed=10519406;
Khelifa T., Rene B., Le Mee S., Lambert B., Saucier J.M.,
Markovits J., Jacquemin-Sablon H., Jacquemin-Sablon A.;
"Transfection of 9-Hydroxyellipticine-resistant chinese hame
fibroblasts with human Topoisomerase Halpha cDNA selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00204; DNA gyraseB; 1. Pfam; PF00521; DNA topoisoIV; 1. Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restoration of the sensitivity to DNA religation inhibitors."; Cancer Res. 59:4927-4936(1999).
-I- FUNCTION: Control of topological states of DNA by transient
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00177; TOPÓISOMERASE_II; 1.
ATP-binding; DNA-binding; Isomerase; Topoisomerase
SEQUENCE 1526 AA; 173156 MW; 9E0CE6B8233CCBCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00434;
                                                                                                                                                                                                                                                                                              Similarity
9; Conser
                                                                                                                                                                                              FLYDDNQRV
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Conservative Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOP4c;
                                                                                                                                                                                                835
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                                                                                                                                                                                                                                                                                              Score 49; DB 2; Length 1526; Pred. No. 1.8; ; Mismatches 0; Indels
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TP2A_MOUSE
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CC -!- SIMILARITY: Belongs to the type II topoisomerase family.

EMBL; Y16595; CAA76313.1; -.

BMED; Y16595; CAA76313.1; -.

RGO; GO:0005634; C:nucleus; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000577; F:NA binding; IEA.

GO; GO:0003677; F:NA binding; IEA.

GO; GO:0003653; F:NA binding; IEA.

GO; GO:0003653; F:NA binding; IEA.

GO; GO:0003653; F:NA binding; IEA.

RGO; GO:0003653; F:NA binding; IEA.

RGO; GO:0003653; F:NA binding; IEA.

RGO; GO:000398; F:NA binding; IEA.

RGO; GO:0003653; F:NA binding; IEA.

RGO; GO:0003653; F:NA binding; IEA.

RGO; GO:000398; F:NA binding; IEA.

RGO; GO:0003997; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

RGO; GO:0003997; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

RGO; GO:000398; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

RGO; GO:000398; F:NA topoisomerase (ATP-hydrolyzing) activity; IEA.

RINETPRO; IPR00394; ATPDING ATPAse.

InterPro; IPR00394; ATPDING ATPAse.

InterPro; IPR00397; CBAR NFYB topis.

InterPro; IPR00141; DNA topoisoIV; 1.

Pfam; PP005204; DNA topoisoIV; 1.

Pfam; PP005204; DNA topoisoIV; 1.

Pfam; PP00521; DNA topoisoIV; 1.

PFAM; PR00418; TP12FAMILY.

DR PRINTS; PR00418; TP12FAMILY.

DR PRINTS; PR00418; TP12FAMILY.

DR PRODOm; PD00074; DNA topoisoIV; 1.

PRODOm; PD00074; DNA topoisoIV; 1.

PRODOM; PD00074; DNA topoisoIV; 1.

R PRODOM; PD00074; DNA topoisoIV; 1.

R PRODOM; PD00074; DNA topoisoIV; 1.

DR PRINTS; SM00433; TOP2C; 1.

DR PRODOM; PD00074; DNA topoisoIV; 1.
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Best Local
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                                                                                                                                                                                                                  TP2A MOUSE STAN
Q01320;
01-APR-1993 (Rel. 2
01-APR-1993 (Rel. 2
05-JUL-2004 (Rel. 4
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                           Name=Top2a; Synonyms=Top2,
Mus musculus (Mouse).
                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
DNA topoisomerase II, alpha isozyme (EC 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00177; TOPOISOMERASE_II; 1.
ATP-binding; DNA-binding; Isomerase; Topoisomerase.
SEQUENCE 1526 AA; 173097 MW; 5E73723C87019929 C
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Delaporte C., Lambert B., Le Mee S., Chaminade F., Sauc:
Jacquemin-Sablon A.;

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: Control of topological states of DNA by the Control of topological states of DN
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DNA topoisomerase II alpha (EC 5.99.1.3).
Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Cranilata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         827
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                           on update)
(EC 5.99.1.3).
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Best Local
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EMBL; U01915; AAC52135.1; -.

PIR; JS0703; JS0703;

HSSP; P06786; 1BJT.

MGD; MGI:98790; TOp2a.

GO; GO:0000793; C:condensed chromosome; IDA.

GO; GO:0005730; C:nucleolus; IDA.

GO; GO:003261; P:chromosome condensation; IMP.

GO; GO:0007059; P:chromosome segregation; IMP.

GO; GO:0007059; P:chromosome segregation; IMP.

GO; GO:0007059; P:chromosome segregation; IMP.

GO; GO:0007059; ATPDING ATPABE.

InterPro; IPR003594; ATPDING TOP36.

InterPro; IPR003595; DNA topoisoIV.

InterPro; IPR003205; DNA topoisoIV.
                                                                                                                                                                                                           Pfam; PF00204; DNA GYPAB-B; 1.
Pfam; PF00521; DNA TOPOSOIV; 1.
Pfam; PF02518 HATPase C; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TP12FAMILY.
PRODOM; PD000742; DNA TOPOSOIV; 1
SMART; SM00387; HATPase C; 1.
SMART; SM00433; TDP2C; 1.
                                                                                                           NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                     SMART; SM00434; TOP4C; 1.

PROSITE; PS00177; TOPOISOMERASE II; 1.

PROSITE; PS00177; TOPOISOMERASE II; 1.

ATP-binding; DNA-binding; Isomerase; Nuclear protein; Topoisomerase.

ATP (Potential).

ATP (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA transcript encoding topoisomerase IIalpha and the receptor alpha locus.; receptor alpha locus.; Cancer Res. 53:5885-5889(1993).
-- PUNCTION: Control of topological states of DNA by breakage and subsequent rejoining of DNA strands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherson J., Brown G.A., Goldenberg G.J.;

"Characterization of a DNA topoisomerase IIalpha gene rearrangement incharacterization of a DNA topoisomerase IIalpha gene rearrangement incharacterization of a fusion messenger and rearrangement encoding topoisomerase IIalpha and the retinoic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi N., Miyaike M., Ikeda H., Kikuchi A.; "Characterization of CDNA encoding the mouse DNA topoisomerase II that can complement the budding yeast top2 mutation."; Nucleic Acids Res. 20:5297-5303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=93065194; PubMed=1331984;
                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: Eukaryotic topoisomerase I and II can inegative and positive supercoils, whereas prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relax only negative supercoils. SIMILARITY: Belongs to the type II topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of double-stranded DNA. SUBUNIT: Homodimer.
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CATALYTIC ACTIVITY: ATP-dependent breakage,
                                      9; Conserv
FLYDDNQRV 9
                                          Conservative
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Pred.
                                                                                                          cleavage (By similarity)
9061778DCA6C756A CRC64;
                                                        49;
No.
                                                        DB
1.8;
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                                                                         Length 1528;
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Topoisomerase
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RESULT 11
TP2A_HUMAN
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P11388; Q9HB24; Q9HB25; Q9HB26; Q9UP44; Q9UU
01-JUL-1989 (Rel. 11, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
DNA topoisomerase II, alpha isozyme (EC 5.9
Name=TOP2A; Synonyms=TOP2;
                                                                                                                                                                                                                                                                                                                                                                "Two diffe
       MEDLINE=91352047; PubMed=1652758;
Bugg B.Y., Danks M.K., Beck W.T., Suttle D.P.;
"Expression of a mutant DNA topoisomerase II in CCRF-CEM leukemic cells selected for resistance to teniposide.";
Proc. Natl. Acad. Sci. U.S.A. 88:7654-7658(1991).
                                                                                                                                                                                                                                                           NUCLEAR EXPORT SIGNAL.
MEDLINE=22705291; PubMed=12821127; DOI
MIRSHI S.E., Bielawski J.C., Cole S.P.
"Identification of functional nuclear
topoisomerase IIalpha and beta.";
                                                                                                                                                                                      VARIANT AMSACRINE-RESISTANT LYS-487.
MEDLINE=91339166; PubMed=1651812;
Hinds M., Deisseroth K., Mayes J., A
                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=99196712; PubMed=10095062; DOI=10.1016/S0167-4781(99)00020-2;
Sng J.H., Heaton V.J., Bell M., Mani P., Austin C.A., Fisher L.M.;
"Molecular cloning and characterization of the human topoisomerase
"Isalpha and IIbeta genes: evidence for isoform evolution through gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93338672; PubMed=8393377;
Tsai-Pflugfelder M., Wang J.C.;
Unpublished results, cited by:
Wasserman R.A., Austin C.A., Fisher
Cancer Res. 53:3591-3596(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).

MEDILNE=89017161; PubMed=2845399;
Tsai-Pflugfelder M., Liu L.F., Liu A.A., Tewey K.M., Whang-Peng J.,
Tsai-Pflugfelder M., Croce C.M., Wang J.C.;
Knutsen T., Huebner K., Croce C.M., Wang J.C.;
Knutsen T., Huebner K., Croce C.M., Wang J.C.;
Clonling and sequencing of cDNA encoding human DNA topoisomerase II
and localization of the gene to chromosome region 17q21-22.";
proc. Natl: Acad. Sci. U.S.A. 85:7177-7181(1988).
                                                                                                              topoisomerase II.";
Cancer Res. 51:4729-4731(1991).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-500 FROM N.A. (
Petruti-Mot A.S., Earnshaw W.
"Two differentially spliced f
mRNAs are conserved between b
                                                                                                                                                                                                                                                                                                                                                                                                                                       duplication.";
Biochim. Bioph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99013880; PubMed=9795238; Lang A.J., Mirski S.E., Cummings "Structural organization of the h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
MEDLINE=99013880;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                   VARIANT TENIPOSIDE-RESISTANT GLN-450.
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                                                                                                                                           namud
FUNCTION:
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                                                                                                                             leukemia cell line merase II.";
                                                                                                                                                                        D.
                                                                                                                                                                                                                                              Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys. Acta 1444:395-406(1999)
                                                                                                                                                                     1339166; PubMed=1651812;
Deisseroth K., Mayes J., Altschuler E.,
D., Zwelling L.A.;
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M., Wang J.C.;
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topological
                                                                                                                                          mutation in the topoisomerase II gene from containing an amsacrine-resistant form of
                                                                                                                                                                                                                                                                                                                                               forms of topoisomerase birds and humans."; EMBL/GenBank/DDBJ data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    н.ј.,
                                                                                                                                                                                                                                                                                                       DOI=10.1016/S0006-291X(03)01077-5;
states
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3C 5.99.1.3).
                                                                                                                                                                                                                                                                            export
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얁
                                                                                                                                                                                                                                                                           sequences
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DNA by transient
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                                             s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL Buropean Bioinformatics Institute. There are no restrict Buropean Bioinformatics Institute. There are more than the by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                    agent ameacrine.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION:
                                                                                                                                                                               ISOId=P11388-4; Sequence=VSP 006530; MISCELLANEOUS: Eukaryotic topolsomerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                      makes double-strand breaks.
CATALYTIC ACTIVITY: ATP-dependent
of double-stranded DNA.
ENZYME REGULATION: Specifically in
                                                                                                                                SIMILARITY: Belongs to the type II topoisomerase
                                                                                                                                                 negative and positive relax only negative
                                                                                                                                                                                                                                                     Name=3
                                                                                                                                                                                                                                                                                   Name=2
                                                                                                                                                                                                                                                                                                                                                      in the nucleoplasm.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breakage and subsequent rejoining
                                                                                                                                                                                                                      Name=4;
                                                                                                                                                                                                                                                                                                                                        Event=Alternative
                                                                                                                                                                                                                                    IsoId=P11388-3;
                                                                                                                                                                                                                                                                     IsoId=P11388-2;
                                                                                                                                                                                                                                                                                                      IsoId=P11388-1;
                   requires a
                               non-profit institu
                                                                                                                                                                 positive supercoils, whereas
                   license
                                                                                                                                                                                                                                                                                                      Sequence=Displayed;
                                                                                                                                                                                                                                Sequence=VSP_006529;
                                                                                                                                                                                                                                                                 Sequence=VSP_006531;
                                                                                                                                                                                                                                                                                                                                      splicing;
                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic
                 agreement
                             is not removed
                                                                                                                                                                                                                                                                                                                                        Named
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f
               Noved. Usage by and to (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                        isoforms=4;
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                                                                                                                                                                                                                                                                                                                                                                                       nuclear;
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EMBL; AF285158; AAG1
EMBL; AF285159; AAG1
PDB; 1LWZ; Model; A-
Genew; HGNC:11989; 7
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                                                                                                                              ; GO:0005634;
; GO:0003677;
; GO:0003918;
                                                                                                                                                                                                                                                         126430;
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AJ011742;
AJ011743;
AJ011744;
AJ011745;
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AF071746;
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AF071747; AAC7731
005634; C:nucleus; TAS.
003677; F:DNA binding; TAS.
003918; F:DNA topoisomerase (A')
1 IPR003594; ATPbind ATPsae.
1; IPR003957; CBFA NFTB topis.
2; IPR001241; DNA topoisoII.
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AAGI 3405
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AAG13405.1; -.; A=431-1252.
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                                                                                                                                       (ATP-hydrolyzing) activity;
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RESULT 12
TP2A_PIG
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Best Local
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                                                                                                                                                                                                                                                                    DNA topoisomerase Name=TOP2A;
                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
05-JUL-2004 (Rel.
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             \frac{1}{1}
                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                    Sus scrofa (Pig).
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SMART; SM00387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF02518; HATPase_c; 1.
                                                           +
                                                                                                                         Submitted (DEC-1997) to
                                                                                                                                             Ito
                                                                                                                                                          SEQUENCE FROM :
TISSUE=Muscle;
                                                                                                                                                                                                     NCBI_TaxID=9823;
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PUNCTION: Control of topological states of DNA by transless, breakage and subsequent rejoining of DNA strands. Top makes double-strand breaks.

CATALYTIC ACTIVITY: ATP-dependent breakage, passage a of double-stranded DNA.

SUBUNIT: Homodimer.

MISCELLANEOUS: Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                   PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 828
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SM00433; TOP2c; 1
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PR00418; TPI2FAMILY.
PD000742; DNA_topoisoIV;
M00087; HATPASE_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                       FROM N.A.
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                      Chordata; Crania:
Cetartiodactyla;
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
alpha isozyme (EC 5.99.1.
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                                                                                                                                                                                                                                                                                                                                     Created)
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cells).
/FIId=VAR 007532.
/FIId=VAR 007533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DE
Pred. No. 1.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_006529.
Q -> QRELCNGAILAHCNLRLMGSSDSPASASRVAGIAGG
CHHTQLIFVFLVETGFHHVGQAGLERLTSGDPPASASQSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear export signal.

DNA cleavage (By similarity).

K -> KSSKYWSSRKSKQHILLNFFVLFKFINDAFFGICPF
                                                                                                                                                                                                                   Craniata; Vertebrata;
actyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (Potential)
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Ref. 4).
Ref. 4).
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Ref. 4).
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Sus.
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                                                                                         transient
Topoisomerase
                                                           and
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RESULT 13
TP2A_CHICK
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Best Local
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Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF00518; HAIPase c; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TP12FAMILY.
PRODOM; PR004742; DNA_topoisoIV; 1
SWART; SW00387; HAIPase_c; 1.
SWART; SW00433; TOP2c; 1.
SWART; SW00434; TOP2c; 1.
                                                                                                                                                                                                                                                                                                15-JUL-1998
16-OCT-2001
05-JUL-2004
                                                                                                           MEDLINE=21346110; PubMed=11453553;
Niimi A., Suka N., Harata M., Kikuchi A., Mizuno S.;
"Co-localization of chicken DNA topoisomerase IIalpha, with sites of DNA replication and possible involvement region of alpha through its binding to PCNA.";
Chromosoma 110:102-114(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                         DNA topoisomerase II, al
Name=TOP2A;
Callus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                      TP2A_CHICK
042130;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003594; ATPbind ATPase. InterPro; IPR003957; CBFA NFVB topis. InterPro; IPR001241; DNA_topoisoIV. InterPro; IPR0012205; DNA_topoisoIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB009387; BAA23778.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
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                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                     Archosauria;
                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00177; TOPOISOMERASE II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P06786; 1BJT
                                                          FUNCTION: Control of topological states of DNA breakage and subsequent rejoining of DNA strand makes double-strand breaks (By similarity).

CATALYTIC ACTIVITY: ATP-dependent breakage, pas
                                    of double-stranded DNA.
SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              negative and positive supercoils, whereas prokaryotic enzymes relax only negative supercoils.
SIMILARITY: Belongs to the type II topoisomerase family.
                       SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
            nucleoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                               828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institu
and this statement
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Eukaryotic topoisomerase I
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                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
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05 DNA cleavage (By similarity)
174306 MW; 529782573BCA6BD2 CRC64;
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Last annotation
alpha isozyme ()
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                        Nuclear;
                                                                                                                                                                                                                                                                                   sequence update)
annotation update)
isozyme (EC 5.99.1.3).
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Pred. No.
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                       generally
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Topoisomerase
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of a C-termin
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RESULT
Q9DFB7
RA Petruti-Mot A.S., Earnshaw W.C.;
RI Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC -I-FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -I-CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -I-SUBUNIT: Homodimer (By similarity).
CC -I-SUBUNIT: Homodimer (By similarity).
CC -I-MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -I-SUMILARITY: Belongs to the type II topoisomerase family.
DR HSSP; P06786; 1BJT.
DR GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003594; ATPbind ATPase.

InterPro; IPR003957; CBPA NPYB topts.

IR InterPro; IPR001241; DNA topoisoII.

InterPro; IPR001265; DNA topoisoIV.

Pfam; PP00521; DNA topoisoIV; 1.

R Pfam; PP00521; DNA topoisoIV; 1.

R Pfam; PP00521; DNA topoisoIV; 1.

R PINTS; PR00615; CCAATSUBUNTA.

PRINTS; PR00615; CCAATSUBUNTA.

PRINTS; PR00615; TP12FAMILY.

R ProDom; PD000742; DNA topoisoIV; 1.

SMART; SM00437; HATPase c; 1.

SMART; SM00433; TOP2c; 1.

SMART; SM00434; TOP4c; 1.

R SMART; SM00434; TOP4c; 1.

R PROSITE; PS00177; TOPOISOMERASE I; 1.

R PROSITE; PS00177; TOPOISOMERASE II; 1.

R PROSITE; PS00177; TOPOISOMERASE II; 1.

PROSITE B006 DNA cleavage (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
Topoisomerase II alpha-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=TOP2A;
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SIMILARITY: Belongs to the type II topoisomerase family.
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9; Conserv
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RESULT
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Q71UH4;
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PRINTS; PRO0615; TCZAATSUBUNTA.

PRINTS; PRO0618; TPIZFAMILY.

PRODOM; PD104963; DNA, topoisoIV; 1.

PRODOM; PD100742; DNA, topoisoIV; 1.

SMART; SM00433; TOP2c; I.

SMART; SM00434; TOP4c; 1.

PROSITE; PS00177; TOPOISOMERASE II; 1.

PROSITE; PS00177; TOPOISOMERASE II; 1.

ATP-binding; DNA-binding; IsomeTase; Topoisomerase.

SEQUENCE 1586 AA; 178839 MW; 422CF3AAC60EA8B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005524; F:ATP binding; IEA.
GO; GO:00057; F:DNA binding; IEA.
GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing)
GO; GO:0003918; F:isomerase activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0006265; F:DNA topoisogical change; IEA.
InterPro; IPR003954; ATPBind ATPAsse.
InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR001258; DNA_GYBSE.
InterPro; IPR001259; DNA_GOPOISOIV.
InterPro; IPR002205; DNA_GOPOISOIV.
                                                                                                                                                                                                           MEDIJINE=99013880; PubMed=9795238;
Lang A.J., Mirski S.E., Cummings H.J., Yu Q., Gerla
"Structural organization of the human TOP2A and TOP
Gene 221:255-266(1998).
-I- FUNCTION: Control of topological states of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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Mammalia; Eutheria;
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MEDLINE=99013880;
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                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                        AF087146;
AF087147;
AF087148;
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                                                                      AF087144;
AF087145;
                    AF087149;
AF087150;
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AF087143;
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PF00521; DNA_topoisoIV; 1.
PF02518; HATPase_C; 1.
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                   AAC77432.1;
AAC77432.1;
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AAC77432.1;
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AAC77432.1;
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Primates;
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Pred. No.
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                                                                                                                 II topoisomerase
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                                                                                                                                                                                                                                 TOP2A and TOP2B genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1586;
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Topoisomerase II
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DR EMBL; AF087153; AAC77432.1; JOINED.

DR EMBL; AF087154; AAC77432.1; JOINED.

DR EMBL; AF087155; AAC77432.1; JOINED.

DR EMBL; AF087155; AAC77432.1; JOINED.

DR EMBL; AF087156; AAC77432.1; JOINED.

DR EMBL; AF087159; AAC77432.1; JOINED.

DR HITCEPTO; IFR001559; AAC77432.1; JOINED.

DR InterPro; IFR001559; AAC77432.1; JOINED.

DR InterPro; IFR001559; DNA_TOPDISOIV.

DR Pfam; PP00214; DNA_TOPDISOIV.

DR Pfam; PP00214; DNA_TOPDISOIV.

DR PFAM; PP00512; DNA_TOPDISOIV.

DR PAINTS; PR00613; TOPAC1.1.

DR PAINTS; PR00613; TOP
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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22.483 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
       _6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
                  US-09-876-889-347
US-09-998-598-2593
US-10-171-311-2522
4 US-10-301-822-211
5 US-10-435-696-46
7 US-10-723-860-2100
5 US-10-296-115-1161
6 US-10-408-765A-3017
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US-10-087-192-477
US-10-087-192-480
US-10-471-758-2
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Sequence 4, Appli
Sequence 477, App
Sequence 480, Appli
Sequence 2, Appli
Sequence 2593, App
Sequence 2523, App
Sequence 211, Appl
Sequence 2100, App
Sequence 1161, App
Sequence 1161, App
Sequence 1161, App
Sequence 3017, App
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67.3	67.3	67.3	67.3	٠	9		69.4	69.4	9	69.4		69.4	69.4	69.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4		71.4	71.4	71.4	٠	75.5	5	81.6	81.6
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US-09-972-656-130	-10-453-		US-10-767-701-48543	-761-7	63-1	-963-11888	US-10-437-963-116905	0-739	626-	-10-425-115-35146	-10-425-	-10-425-115-28441	-10-767-701-	-10-424-599-18291	-10-437-963-	-10-282-122A-	-10-156-	0-282-122A-	-493-2	-114-5389	0-425-115-	-10-425-115-	-10-369-493-	-10-437-963-10962	-10-282-122A-690	-10-425-114-	-10-437-963-1622	-10-779-4	-10-779-461-	US-10-369-493-5597	US-10-369-493-5596
130,	Sequence 117, App	e 117,	Sequence 48543, A	e 7834,	e 1723	e 1188	Sequence 116905,	e 1019	_	Sequence 351466,	æ	æ	æ	Ø	e 18978	e 68528,	e 9305	æ	e 20595,	Sequence 53896, A	Sequence 347738,	e 295784		10962	e 69	e 47(	e 16	e 51,	e 11,	e 5597,	96

# ALIGNMENTS

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APPLICANT: Namakrishna, Venky
APPLICANT: Philip, Ramila
TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Treat
TITLE OF INVENTION: Diagnosis of Cancer
FILE REFERENCE: 26747-35
CURRENT APPLICATION NUMBER: US/10/006,177
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US/60/251,022
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-00
SOPTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 9
TYPET
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                                                                                                                                                 ; OTHER INFORMATION: Epitopic Peptide US-10-006-177-4
                                                                 Best Local :
Matches 5
                                                                                          Query Match
Best Local (
                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                     1 FLYDDNQRV 9
                                                                     h 100.0%; Score 49; DB 14; Similarity 100.0%; Pred. No. 1.5e+06; 9; Conservative 0; Mismatches 0;
FLYDDNQRV 9
                                                                                                        Length 9;
                                                                       Indels
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                                                                       Gaps
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FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 480
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US-10-471-758-2
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Sequence 2, Application US/10471758
Publication No. US20040249574A1
GENERAL INFORMATION:
APPLICANT: Tishby, Naftali
APPLICANT: Seldin, Yevgeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 477
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Best Local Similarity
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Best Local Similarity 100.0%;
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MORRIS, David W.
APPLICANT: Engelhard, Bric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1083
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 13; 100.0%; Pred. No. 1.7;
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Pred. No. 1.5;
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APPLICANT: Benson, Darin R.

APPLICANT: Lodes, Michael J.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS FILE REPERENCE: 210121.466C3

CURRENT APPLICATION NUMBER: US/09/876,889

CURRENT APPLICATION NUMBER: US/09/876,889

NUMBER OF SEQ ID NOS: 353

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 347
                                                                             ; Sequence 2593, Application US/09998598
; Patent No. US20020159922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT APPLICATION SONTE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                US-09-998-598-2593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-876-889-347
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CURRENT APPLICATION MUMBER: US/10/471,758
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 1526
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Cortxa Invention Disclosure Database
SEQ ID NO 2593
LENGTH: 1531
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Best Local :
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Best Local Similarity
Matches 9; Conserv
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Patent No. US20020076715A1
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TYPE: PRT
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Local Similarity 100.0%; Pred. No. 2.4;
1e8 9; Conservative n. Mineralis
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ilarity 100.0%; Pred. No. 2..
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                            US-10-301-822-211
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Sequence 211, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 222, Application US/10171311 Publication No. US20030087270A1
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Best Local :
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                       APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L.
                    APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS:
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
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CURRENT APPLICATION NUMBER: US/10/301,822
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es 9; Conserv
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Schlegel, Robert
Monahan, John E.
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Zhao, Xumei
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Gannavarapu, Manjula
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Kamatkar, Shubhangi
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100.0%; Pred. No. 2.4;
vative 0; Mismatches
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                                                        ASSESSMENT, PREVENTION,
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US-10-723-860-2100
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US-10-435-696-46
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US-10-435-696-46
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PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                            Sequence 2100, Application US/10723860 Publication No. US20040253606A1 GENERAL INFORMATION:
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LENGTH: 1531
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Publication No.
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Co
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma
FILE REFERENCE: 05882 0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT APPLICATION NUMBER: 00/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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APPLICANT: Munnes, Marc
APPLICANT: Munnes, Marc
APPLICANT: Kallabis, Harald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSI
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REFERENCE: LeA 36 108
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP03003112.4
PRIOR FILING DATE: 2003-02-13
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NUMBER OF SEQ ID NOS: 314
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TYPE: PRT
ORGANISM: Homo Sapiens
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Similarity 100.0%;
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Pred. No. 2.4;
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Query Match
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US-10-296-115-1161
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US-10-723-860-2100
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
FILE REPERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1161
LENGTH: 1621
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3017
LENGTH: 1626
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GENERAL INFORMATION:
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SOFTWARE: PatentIn version
SEQ ID NO 2100
LENGTH: 1531
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Best Local
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                                                                                                          APPLICANT: WARNOCK, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                        APPLICANT: Ghosh, Soumitr
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(1621)
OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                INFORMATION:
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Similarity 100.0%;
9; Conservative 0
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Taylor, Steven W.
Glenn, Gary M.
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Pred. No. 2.6;
0; Mismatches
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Pred. No. 2.4;
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US-10-369-493-5596
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TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5435
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US-10-369-493-5435
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                                                                                         ; ORGANISM: Caenorhabditis elegans US-10-369-493-5596
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                                                                                                                                                   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 5596 LENGTH: 1520
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GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative 0,
Query Match 81.6%; Score 40; DB 14; Length 1520; Best Local Similarity 66.7%; Pred. No. 1.2e+02; Matches 6; Conservative 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FLYDDNQRV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FLYDDNQRV 9
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49;
Pred. No.
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RESULT 15
US-10-369-493-5597
US-10-369-493-5597
Sequence 5597, Application US/10369493
Publication No. US20030233675A1
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao; Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION BATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5597
CENGTH: 1520
TYPE: PRI
ORGANISM: Caenorhabditis elegans
US-10-369-493-5597
Search completed: December 29, 2004, 16:42:49 Job time : 145 secs
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                                                                                                                                                                                     Query Match 81.6%; Score 40; DB 14; Length 1520; Best Local Similarity 66.7%; Pred. No. 1.2e+02; Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                          863 FLYBENQRI 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      863 FLYEENQRI 871
                                                                                                                                          1 FLYDDNORV 9
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                                                                                                                                                                                          0; Gaps
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 16:21:45; Search time 38 Seconds (without alignments)
22.788 Million cell updates/sec

Title: US-10-006-177-4
Perfect score: 49
Sequence: 1 FLYDDNQRV 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

# SUMMARIES

Result No.	Score	Query Match	Length	DВ	ID	Description
ב :	49	100.0	227	2	A48536	DNA topoisomerase
N	49	•	227	N	v	
w	49	8	1526	N	JN0598	
4	49	8	1526	N	A44406	
ហ	49	•	1528	N	JS0703	•
თ	49	•	1530	N	A40493	
7	49		1612	N	S59969	
8	49	100.0	1626	N	A39242	
9	41	83.7	558	N	AE1236	glycerol 3 phospha
10	40	81.6	816	N	C88196	protein ZK1127.7 [
11	40	•	1520	N	T23620	hypothetical prote
12	37		80	N	T00184	
13	37		82	N	G89987	hypothetical prote
14	37	75.5	112	μ.	L6HUAR	Ig lambda chain V-
15	36	٠	329	N	T21844	hypothetical prote
16	36	•	968	N	D87570	
17	36	73.5	1711	N	T18429	S
18	35	•	558	N	AB1599	:3
19	35	71.4	659	N	F70175	36
20	35	71.4	869	N	T35162	nsketolase
21	34	69.4	88	N	H89858	conserved hypothet
22	34	69.4	102	μ	HSTE41	histone H4, major
23	34	69.4	102	<u>.</u> .	HSTE42	Η4,
24	34	69.4	103	N	A25875	histone H4 - Tetra
25	34	69.4	151	N	A97008	
26	34	9	229	N	T09824	fiber protein 3 (i
27	34	69.4	252	N	AI1378	
28	34	69.4	252	N	AB1748	acetylesterase hom
29	34	69.4	275	N	T09822	fiber protein 2 [i

Query Match 100.0%; Score 49; DB 2; Length 227; Best Local Similarity 100.0%; Pred. No. 0.044; Matches 9; Conservative 0; Mismatches 0; Indels

0; Gaps

0;

BASSILT 2 B48536 C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 16.Feb-1994 #sequence_revision 18-Nov-1994 #text C;Date: 16.Feb-1994 #sequence_revision 18-Nov-1994 #text C;Accession: B48536 R;Tsutsui, K.; Tsutsui, K.; Okada, S.; Watanabe, M.; Sh J, Biol. Chem. 268, 19076-19983, 1993 A;Title: Molecular cloning of partial cDNAs for rat DNA A;Title: Molecular cloning of partial cDNAs for rat DNA A;Reference number: A48536; MUID:93366832; pMID:8395528 A;Accession: B48536 A;Status: preliminary A;Status: preliminary A;Cross-references: UNIPROT:Q63177 A;Cross-references: UNIPROT:Q63177 A;Cross-references: UNIPROT:Q63177 A;Experimental source: Sprague-Dawley, brain A;Note: sequence extracted from NCPI backbone (NCBIN:13) C;Superfamily: eukaryotic type II DNA topoisomerase; ph	Best Local Similarity 100.0%; Pred. No. 0.044; Matches 9; Conservative 0; Mismatches  Qy 1 FLYDDNQRV 9           Db 91 FLYDDNQRV 99	oisomerase II type A - rat (fragment) es: Rattus norvegicus (Norway rat) 16-Feb-1994 #sequence_revision 18-Nov-199 sion: A48536 ui, K.; Tsutsui, K.; Okada, S.; Watanabe, Chem. 268, 19076-19083, 1993 : Molecular cloning of partial cDNAs for x ence number: A48536; MUID:93368832; PMID:8 sion: A48536 s: preliminary ule type: nucleic acid ule type: nucleic acid ules: 1-227 <tsu> imental source: Sprague-Dawley, brain sequence extracted from NCBI backbone (NC family: eukaryotic type II DNA topoisomera rds: ATP</tsu>	ALIGNMENTS	30 34 69.4 307 2 S75461 31 34 69.4 331 2 T09820 32 34 69.4 485 2 C64680 33 34 69.4 494 2 S75398 34 34 69.4 618 2 T28666 35 33 67.3 88 2 H84078 36 33 67.3 131 1 L6HUEB 37 33 67.3 294 2 D85016 39 33 67.3 294 2 D85016 39 33 67.3 393 2 T21295 40 33 67.3 396 1 B69851 41 33 67.3 410 2 T06665 42 33 67.3 476 2 T46067 43 33 67.3 573 2 H89904 45 33 67.3 573 2 H89904
1994 #text_change 09-Jul-2004 e, M.; Shohmori, T.; Seki, S.; Inoue, Y. r rat DNA topoisomerase II isoforms and t D:8395528 (NCBIN:136743, NCBIP:136746) erase; phage T4 DNA topoisomerase (ATP-hy	0; Indels 0; Gaps 0;	Shohmoz Shohmoz DNA topo 528 528 ;:136742, phage T		hypothetical prote fiber protein 1 [i hypothetical prote lysine-tRNA ligase hypothetical prote hypothetical prote hypothetical prote la lambda chain protein - hypothetical prote hypothetical prote cytochrome P450 yi hypothetical prote fumarylacetoacetas hypothetical prote aerobic glycerol-3 probable primosoma

FLYDDNQRV

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CiSpecies: Rattus norvegicus (Norway rat)
CiDate: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 16-Jul-1999
CiAccession: JN0598; 332012
RiPark, S.H.; Yoon, J.H.; Kwon, Y.D.; Park, S.D.
Biochem. Biophys. Res. Commun. 193, 787-793, 1993
A;Title: Nucleotide sequence analysis of cDNA for rat DNA topoisomerase A;Reference number: JN0598; MUID:93290677; PMID:8390253
A;Accession: JN0598
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
                                                                              RESULT 5
JS0703
DNA topolsomerase (ATP-hydrolyzing) (EC 5.99.1.3) II -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: sequence extracted from NCBI backbone (NCBIP:123211)
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase
C;Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: nucleic acid
A;Residues: 1-1526 <CHAP
A;CResidues: 1-1526 <CHAP
A;CZOSS-references: UNIPROT:P41515; GB:L04607; NID:g191217; PIDN:AAA37023.1;
A;Experimental source: ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A44406
R;Chan, V.T.; Ng, S.W.; Eder, J.P.; Schnipper, L.E.
J. Biol. Chem. 268, 2160-2165, 1993
A;Title: Molecular cloning and identification of a point A;Reference number: A44406; MUID:93131977; PMID:8380592
A;Accession: A44406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA topoisomerase (ATP-hydrolyzing) (BC 5.99.1.3) - Chine N;Alternate names: DNA-gyrase; type II DNA topoisomerase C;Species: Cricetulus griseus (Chinese hamster) C;Datc: 31-Dec-1993 #text_C;Datc: 31-Dec-1993 #text_C;Datc: 31-Dec-1993 #text_Cricetian Page 1998 | Cricetian Page 1998 | C
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A;Cross-references: EMBL:Z19552; NID:g57963; PIDN:CAA79611.1; PID:g57964
A;Experimental source: trestis
A;Note: the authors translated the codon GTG for residue 3 as Leu
C;Comment: This enzyme is required for the segregation of circular DNA molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3);Alternate names: DNA topoisomerase II
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Best Local
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                                                                                       mouse
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        09-Jul-2004
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        RESULT
S59969
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A; Molecule type: mRNA
A; Residues: 1-1530 < TSA>
A; Cross-references: GB:J04088
A; Cross-references: GB:J04088
R; Bugg, B.Y.; Danks, M.K.; Beck, W.T.; Suttle, D.P.
Proc. Natl. Acad. Sci. U.S.A. 89, 7654-7658, 1991
A; Title: Expression of a mutant DNA topoisomerase II in
A; Reference number: A41278; MUID:91352047; PMID:1652758
A; Accession: A41278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: $35483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1528 <ADDA2>
A;Cross-references: EMBL:D12513; NID:g220615; PIDN:BAA02076.1; PID:g220616
A;Cross-references: EMBL:D12513; NID:g220615; PIDN:BAA02076.1; PID:g220616
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisome C;Keywords: ATP: DNA binding; isomerase; leucine zipper; nucleus
F;994-1015/Region: leucine zipper motif
F;804/Active site: Tyr #status predicted
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Nucleic Acids Res. 20, 5297-5303, 1992
A;Title: Characterization of cDNA encoding the mouse DNA topoisomerase II that can compl A;Reference number: S35483; MUID:93065194; PMID:1331984
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R;Adachi, N.; Miyaike, M.; Iked.
submitted to JIPID, July 1992
A;Reference number: JS0703
A;Accession: JS0703
A;Status: translation not shown
                                                                                                                                                          A;Cross-references: GDB:118884; OMIM:126430
A;Map position: 17q21-17q22
C;Superfamily: eukaryotic type II DNA topoi
C;Keywords: ATP; DNA binding; isomerase; nu
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A; Residues: 442-521 <BUG>
A; Note: a mutant with res
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A;Accession: A40493
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A; Residues: 1-1528 < ADA>
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                                                                                                  Local
                                                                                                                                                                                                                                                                                  a mutant with residue 449-Arg replaced by Gln was resistant to teniposide
827
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                                                                                                  100.0%; Score 49; 100.0%; Pred. No.
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100.0%; Pred. No. 0.34;
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isomerase; nucleus
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A;Cross-references: GB.X53662; GB:S56813; NID:g38324; PIDN:CAA37706.1; R;Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M. Blophys. Acta 1172, 283-291, 1993 A;Title: Novel HeLa topoisomerase II is the II-beta isoform: complete c A;Reference number: S30190; MUID:93192319; PMID:8383537 A;Accession: S33970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Austin, C.A.; Fisher, L.M.
FBBS Lett. 26f, 115-117, 1990
A;Title: Isolation and characterization of A;Reference number: S10710; MUID:90306333; A;Accession: S10710
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A39242
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A;Title: Cloning and characterization of full-length cDNAs coding for the large coding for t
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A;Residues: 1-23,29-1610,'A',1612-1626 <AU2>
A;Cross-references: EMBL:Z15111
R;Austin, C.A.; Sng, J.H.; Patel, S.; Pisher submitted to the EMBL Data Library, Septembe
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A;Title: Characterization and immunological identification of cDNA clones ence A;Reference number: A39242; MUID:90083281; PMID:2556712
A;Accession: A39242
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C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; DNA replication; isomerase; nucleus
F;697-927/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4
A;Reference number: S30191
A;Accession: S30191
A;Molecule type: mRNA
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A; Residues: 1043-1276 < AUS>
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;Residues: 1-23,29-1626 <JEN>
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lternate names: DNA topoisomerase II isoform beta; DNA-gyrase
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PMID:2163884
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A;Residues: 596-1430,'S',1432-1610,'A',1612-1626 <AUI>
A;Cross-references: EMBL:Z15115; NID:g288564; PIDN:CAA78821.1; PID:g288565
A;Cross-references: EMBL:Z15115; NID:g288564; PIDN:CAA78821.1; PID:g288565
A;Davies, S.L.; Jenkins, J.R.; Hickson, I.D.
Nucleic Acids Res. 21, 3719-3723, 1993
A;Title: Human cells express two differentially spliced forms of topoisome:
A;Reference number: S41641; MUID:93376494; PMID:8396237
A;Accession: S41641
C;Accession: C88196
R;anonymous, The C. elegans Sequencing
Science 282, 2012-2018, 1998
                                 protein ZK1127.7 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #C;Accession: C88196
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C;Superfamily:
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.;
ok, C.; Schueter, T.; Simoes, N.; Therrez, A.; Vazquez-i
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1236
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A;Residues: 24-80 <DAV>
A;Cross-references: EMBL:X71911; NID:g396540; PIDN:CAA50726.1; PID:g3980296
A;Cross-references: EMBL:X71911; NID:g396540; PIDN:CAA50726.1; PID:g3980296
A;Note: this sequence represents a long minor splice form, designated beta-:
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77.8%;
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Pred. No. 4.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            GB:NC_003210; PIDN:CAC99371.1; PID:g16410709;
                                                                                                                                                                                                                                             Mismatches
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4.2;
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Dussurget, O.;
                                                   #text_change
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                                                     09-Jul-2004
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tian, K.D.;
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Voss, H.; Wehland
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Fsihi, H
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A; Title: Genome A; Reference numb

MUID:99069613; PMID:9851916

platform

for

investigating biolog

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A; Note:
C; Geneti
                                R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Blosci. Biotechnol. Biochem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukocidin genes in a phage-like particle isolated A;Reference number: Z14119; MUID:98067870; PMID:9404084
A;Accession: T00184
                                                                                                                                hypothetical protein 51 - Staphylococcus aureus phage phi PVL
;Species: Staphylococcus aureus phage phi PVL
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
C;Accession: T00184
                                                                                                                                                                                                                                                                                             문
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A; Residues: 1-1520 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: Z19772 A;Accession: T23620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K12D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23620; T28109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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A; Molecule type:
                                                                                                                                                                                                                  T00184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A;Accession: T28109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: Z20470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1520 <WIL>
A; Residues: 1-1520 <WIL>
A; Cross-references: UNIPROT: Q23670;
A; Experimental source: clone K12D12
A; Experimental source: clone K12D12
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                                                                                                                                                                                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: 2
/Map position: 2
/Introns: 34/1; 146/2; 390/3;
// Amarfamily: eukaryotic type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: EMBL;Z70213; PIDN:CAA94177.1; GSPDB:GN00020; CESP:K12D12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated
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                    Status: translated from GB/EMBL/DDBJ
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Best Local :
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Best Local
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published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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66.7%;
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66.7%;
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II DNA topoisomerase; phage '
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Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB
Pred. No. 10;
3; Mismatches
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II
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A; Molecule type: protein
A; Residues: 1-112 <SLES
A; Cross-references: UNIPROT: P01721
A; Note: about half of the lambda chain C r
C; Comment: This protein was isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.
Blochem. J. 195, 561-572, 1991
A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-ch.
A;Reference number: A01987; MUID:82091000; PMID:6797401
A;Contents: amyloid protein AR
A;Contents: amyloid protein AR
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G89987
                                                                                                                                                     A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982
C;Accession: A01987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-82 <KUR>
A;Cross-references: UNIPROT:Q99SR5;
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SA1786 [imported] - Staphylococcus aureus (strain NJID C;Species: Staphylococcus aureus C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                           F;22-91/Disulfide
                                                                                                              C;Keywords: amyloid; heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                        A;Gene: GDB:IGLV@
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.; Shiba, T.; Hattori, M. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-80 <KAN>
A;Cross-references: UNIPROT:O80089; EMBL:AB009866; NID:d1204727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig lambda chain V-VI region (AR) - human (tentative sequence)
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Matches
                      Query Match
Best Local
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                                                                                           #status
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                      75.5%;
85.7%;
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pred. No. 4.6;
1; Mismatches
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Pred. No. 3.3;
2; Mismatches
                                                                                         predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:BA000018; PID:g13701771; PIDN:BAB43064.1; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                      1.6;
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                                             Length 112
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Conservative

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hypothetical protein F36D1.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21844
C;Accession: T21844
R;Harris; B.
Submitted to the EMEL Data Library, November 1996
A;Reference number: Z19477
A;Accession: T21844
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-329 <WIL>
A;Cross-references: UNIPROT:Q9XV37; EMBL:Z81530; PIDN:CAB04310.1; GSPDB:GN00019; CESP:F3
A;Experimental source: clone F36D1
C;Genetics:
A;Gene: CESP:P36D1.8
A;Map position: 1
A;Introns: 60/1; 75/3; 123/2; 167/2; 214/2; 267/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F49D11.3
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Search completed: December 29, 2004, 16:31:13 Job time : 39 secs
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                                                                                                                                                                                                     Query Match 73.5%; Score 36; DB 2; Length 329; Best Local Similarity 85.7%; Pred. No. 23; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                  101 FLYDENQ 107
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